

ફોરેન્સિક રિપોર્ટ

BLASTP ALIGNMENT OF SEQ ID NO: 5 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 5)  
Subject: -gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
Length = 243

Score = 158 (60.7 bits), Expect = 1.3e-08, P = 1.3e-08

Identities = 42/136 (30%), Positives = 67/136 (49%)

Query: 670 RVAFSAA-RTSNLAPGTLDQPIVFDLLNNLNGETFDLQLGRFNCPVNGTYVFIFHMLKLA 728  
R AFS T P + PI F + N +D G+F+C + G Y F +H+  
Sbjct: 111 RSAFSVGLETYVTVP--NMPIRFTKIFYNQQNHYDGSTGKPHCNIPGLYYFAYHITVYM 167

Query: 729 VNVPLYVNLMKNEEVILVSAYANDGAPDHETASNHAIIQLFQGDQIWLRLH----RGAIYG 784  
+V V+L K ++ ++ Y + + AS +L L GDQ+WL++ R +Y  
Sbjct: 168 KDVK--VSLFKKKDAAMLFTYDQYQENNVDQASGSVLJHLEVGDQVWLIQVYGEGERNGLYA 225

Query: 785 SSWKYSTFSGYLYQD 800  
+ STF+G+LLY D  
Sbjct: 226 DNDNDSTFTGFLLYHD 241

FIG. 1

BLASTP ALIGNMENT OF SEQ ID NO: 5 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 5)  
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human

adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 156 (60.0 bits), Expect = 4.3e-09, P = 4.3e-09

Identities = 41/136 (30%), Positives = 67/136 (49%)

Query: 670 RVAFSAAR-TSNLAPGTLLDQPIVFDLILNNLGETFDLQLGRFNCPVNNGTYVFLFHMLKLA 728  
R AFS T P + P F + N +D G+F+C + G Y F +H+

Sbjct: 112 RSAFSVGLETYYTIP--NMPPERFTKIFYNQQNHYDGSTGKPHCNIPGLYYFAYHITVYM 168

Query: 729 VNVPLIYNLMKNEEVLVSAVYANDGAPDHETASNHALQLFQGDQIWLRH---RGAIYG 784  
+V V+L K ++ Y ++ AS +L L GQD+WL++ R +Y

Sbjct: 169 KDVK--VSLFKKKDKAAMLFTYDQYQENNYDQASGSVLLHLEVGDQWVLQVYCEGERNGLYA 226

Query: 785 SSWKYSTFSGYLLYQD 800

+ STF+G+LLY D

Sbjct: 227 DNDNDSTFTGFLLYHD 242

FIG. 2

BLASTP ALIGNMENT OF SEQ ID NO: 15 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 15)  
Subject: gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
Length = 243

Score = 147 (56.8 bits), Expect = 2.6e-07, P = 2.6e-07

Identities = 40/136 (29%), Positives = 65/136 (47%)

Query: 580 RVAFSAAR-TTSNLAPGTLIDQPYGVDLLNNLGETFDLQLGRFNCPVNGTYVFIFHMLKLA 638  
R AFS T P + P + N +D G+F+C + G Y F +H+  
Sbjct: 111 RSAFSVGLETYVTVP--NMPIRFTKIFYNQQNHYDGSTGKPHCNIPGLYYFAZHITYM 167

Query: 639 VNVPLYVNLMKNEEVILVSAYANDGAPDHETASNHAIIQLFQGDQIWLRLH----RGAIYG 694  
+V V+L K ++ ++ Y + + AS +L L GDQ+WL++ R +Y  
Sbjct: 168 KDVK--VSLFKKDAAAMLFTYDQYQENNVDQASGSVLLHLEVGDDQVWLQVYCEGERNGLYA 225

Query: 695 SSWKYSTFSGYLQD 710  
+ STF+G+LLY D  
Sbjct: 226 DNDNDSTFTGFLLYHD 241

FIG. 3

தோலைட் குறிச்சுடுக்கு

BLASTP ALIGNMENT OF SEQ ID NO: 15 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 15)  
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 151 (58.2 bits), Expect = 1.5e-08, P = 1.5e-08

Identities = 40/136 (29%), Positives = 66/136 (48%)

Query: 580 RVAFSAA-RTSNLIAPGTLIDQPYGVDLILNNLGETFDLQLGRNCPVNGTYVFIFHMLKLA 638  
R AFS T P + P + N +D G+F+C + G Y F +H+  
Sbjct: 112 RSAFSVGLETYYTIP--NMPPERFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYM 168

Query: 639 VNVPLYVNLMKNEEVLVSAVANDGAPDHETASNHAIIQLFQGDDQIWLRLH---RGAIYG 694  
+V V+L K ++ ++ Y +++ AS +L L GDD+WL+++ R +Y  
Sbjct: 169 KDVK- -VSLFKKDKAAMLFTYDQYQENNYDQASGSVLLHLEVGDQVWLQVYGEGERNGLYA 226

Query: 695 SSWKYSTFSGYLLYQD 710  
+ STF+G+LLY D  
Sbjct: 227 DNDNDSTFTGFLLYHD 242

FIG. 4

## BLASTP ALIGNMENT OF SEQ ID NO: 28 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 28)  
 Subject: gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 351 (128.6 bits), Expect = 7.7e-31, P = 7.7e-31

Identities = 84/225 (37%), Positives = 124/225 (55%)

Query: 525 GPPGFPGIGKPGVAG-LHGPPGKGALCPQQGPGLPGPPGPPGPPGPPAVMPPPTPPPQGE 583  
 Sbjct : 23 GPGVLLPLPKGACTGWMAGIPGHPGHNGVPGRDGRDGTGEKGDPLIGP---KG- 77

Query: 584 YLPDMG-LGIDGVKPPHAYGAKGKGNGP--AYEM-PAFTAELTAPFPPVGAVPKFNKL 638  
 Sbjct : 78 ---DTGETGVTGAEGPRGFPGIQRKGEPEGAYVYRSAFSVGILETYVTVPNMPIRFTKI 134

Query: 639 LYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGGNNEPVMYTYDEYKKGFLD 698  
 Sbjct : 135 FYNQQNHYDGSTGKFCNCIPGLYYFAYHITVYMKDVKVSLFKDKAMLFTYDQYQENNVD 194

Query: 699 QASGSAVLRLRPDRVFLQMPSE-QAAGLYAGQYVHSSFSGYLLY 742  
 Sbjct : 195 QASGS +L L GD+V+LQ+ E + GLYA S+F+G+LLY

**FIG. 5**

“T O E D I E T ” G E T S O O D T

BLASTP ALIGNMENT OF SEQ ID NO: 28 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 28)  
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 363 (132.8 bits), Expect = 6.7e-33, P = 6.7e-33

Identities = 87/236 (36%), Positives = 129/236 (54%)

Query: 514 I P G P K G E P G L P G P P G F P G I G K P G V A G - L H G P P G K R P G A L G P Q G Q P G Q P G L P G P P G P P A 572  
+ PG E + GP + K G + G PG PG G G+ G PG G G G P  
Sbjct: 13 L P G H D Q E T T I Q G P G V I L L P L P K G A C T G W M A G I P G H P C H N G A P G R D G R D G T P G E K G E K G D P G 72

Query: 573 V M P P T P P P Q G E Y L P D M G - L G I D G V K P P H A Y G A K K G K N G G P -- - A Y E M - P A F T A E L T A P F P 627  
++ P +G D+G G+ G + P + +G+ G P AY AF+ L +  
Sbjct: 73 L I G P -- - K G -- - D I G E T G V P G P A E G P R G F P G I Q G R K G E P G E G A Y V Y R S A F S V G L E T Y Y T 124

Query: 628 P V G A P V K F N K L L Y N G R Q N Y N P Q T G I F T C E V P G V Y Y F A Y H V H C K G G N V W V A L F K N N E P V M Y 687  
P +F K+ YN + +Y+ TG F C +PG+YYFAYH+ +V V+LFK +++  
Sbjct: 125 I P N M P E R F T K I F Y N Q Q N H Y D G S T G K F H C N I P G L Y Y F A Y H I T V Y M K D V K V S L F K K D K A M L F 184

Query: 688 T Y D E Y K K G F L D Q A S G A V I L L R P G D R V F L Q M P S E - Q A A G L Y A G Q Y V H S S F S G Y L L Y 742  
TYD+Y++ DQASGS +L L GD+V+LQ+ E + GLYA S+F+G+LLY  
Sbjct: 185 T Y D Q Y Q E N N Y D Q A S G S V I L L H L E V G D Q V W L Q V Y G E G E R N G L Y A D N D D S T F T G F L L Y 240

FIG. 6

**BLASTP ALIGNMENT OF SEQ ID NO: 160 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)**

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 160)  
 Subject: gi|5213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 410 (149.4 bits), Expect = 5.3e-38, P = 5.3e-38

Identities = 92/228 (40%), Positives = 133/228 (58%)

Query:	53 GPHGRIGLPGRDGRDGRKGEKGKGTAGLRGKTGPLGLAGEKGKDQGETGKGPIGPEGEK 112
Sbjct:	GP + LP G G G+ G+ G G GEKG++G+ G IGP+G+
Query:	23 GPGVLLPLPKGACTGWMAGIPGHPGHNGVPGRDGRDGPGL--IGPKGDT 79
Sbjct:	
Query:	113 GEVGPPIGPGPKGDRGEQGDGPGLPGVCRCGSIVLKSAFSVGITTSYPEERRLPLIFENKVLF 172
Sbjct:	GE G GP+G G QG G PG G+ V +SAFSVG+ T +PI F K+ +
Query:	80 GETGVTGAEGPRGFPGIQRKGEPGE ---GAYVYRSAFSVGLETYVTPNMPIRFTKIFY 136
Sbjct:	
Query:	173 NEGEHYNPATGKFICAFPGIYYFSYDITLANKHLAIGLVHNGQYRIKTFDANTGNH-DVA 231
Sbjct:	N+ HY+ +TGKF C PG+YYF+Y IT+ K + + L + + T+D N+ D A
Query:	137 NQQNHYDGSTGKPFHCNIPGLYYYFAHITVYMKDVVKVSLFKKDKAAMLFTYDQYQENNVDQA 196
Sbjct:	
Query:	232 SGSTVILQPEDEVWLEIFFT-DQNLFSDPGWADSLFSGFLLYVDTD 278
Sbjct:	SGS +++L+ D+VWL++ ++NGL++ DS F+GFLLY DT+ NDSTFTGFLLYHDTN 243

**FIG. 7**

TOEOT "6645000T

BLASTP ALIGNMENT OF SEQ ID NO: 160 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 160)  
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 411 (149.7 bits), Expect = 7.3e-39, P = 7.3e-39

Identities = 94/238 (39%), Positives = 134/238 (56%)

Query: 43 PGPPGANGSPGPGRIGLPGRDGRKGERKTAGLRLGKTPGLGLAGEKGDKQGETGK 102  
PG GP + LP G G G+ G G GEKG+G+ G  
Sbjct: 14 PGHDQETTIQGPVGVLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGTGKGEKGDPGL 73

Query: 103 KGPIGPEGEKGEVGPIGPPGPKGDRGEQQDPGLPGVCRCGSIVLKSAFSVGVITTSYPEER 162  
IGP+G+ GE G GP+G G QG G PG G+ V +SAFSVG+ T Y  
Sbjct: 74 - - -IGPKGDIGETGVPGAEGRGFPGLQGRKGEPE-- -GAYYVRSAFSVGLETYTYTIPN 127

Query: 163 LPIIFNKVLFNEGEHYNPATGKFICAFPGIYYFSYDITLANKHLAIGLVHNGQYRIKTFD 222  
+P F K+ +N+ HY+ +TGKF C PG+YYF+Y IT+ K + + L + + T+D  
Sbjct: 128 MPERFTKIFYNQONHYDGSTGKFHCNIPGLYYFAYHTVYMKDVKVSLFKDKAMLFRTYD 187

Query: 223 A-NTGNHDVASGSTVIYLOPEDEVWLEIFFT-DONGLFSDPGWADSLFSGFLLYVDTD 278  
N+D ASGS + +L+ D+VWL++ +NGL++ DS F+GFLLY DT+  
Sbjct: 188 QYQENNYDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADND-NDSTFTGFLLYHDTN 244

FIG. 8

## BLASTP ALIGNMENT OF SEQ ID NO: 186 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 186)  
 Subject: gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 472 (171.2 bits), Expect = 1.4e-44, P = 1.4e-44

Identities = 104/204 (50%), Positives = 130/204 (63%)

Query: 86 GI|KGDQGSRGSPGKHGPGLAGPMGEKGILRGETGPQQGKGNKGDVGPTGPPEGPRGNIGPL 145  
 GI G G G PG+ G G GEKG G GP KG+ G+ G TG EGPRG G  
 Sbjct: 41 GIPGHPGHNGVPGGRDGTGPKGEKGDPGLIGP--KGDGTGETGVTAEGPRGFPGIQ 97

Query: 146 GPTGLPMPMGPIGKPG-PKG-EAGPTGPQDMPIKFDKILYNEFFNHYDTAACAKFTCHIAGV 203  
 G G PG + + G E T P +MPI+F KI YN+ NHYD + GK F C+I G+  
 Sbjct: 98 GRKGEPEGEGAYVYRSAAFSVGLETYVTVP-NMPIRFTKIFYFNQONHYDGSTGKFHCNIPGL 156

Query: 204 YYFTYHITVFSRNVQVSLLVKNGVKILHTKDAYSSE-DQASGGIVLQLKLGDEVWLQVYTG 262  
 YYF YHITV+ ++V+VSL K +L T D Y + DQASG + +L L+GD+VWLQV G  
 Sbjct: 157 YYFAYHITVYMKDVKVSLFKDKAMLFYDQYQENNTDQASGSVLLHLEVGDQVWLQVYVG 216

Query: 263 -GERFNGLFADEDDDTTFTGELLF 285  
 GER NGL+AD D+D+TFTGELLF+  
 Sbjct: 217 EGER-NGLYADNDNDSTFTGELLFY 239

**FIG. 9**

**BLASTP ALIGNMENT OF SEQ ID NO: 186 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)**

Query:	Adiponectin-Like Polypeptide (SEQ ID NO: 186)	
Subject:	AAY85144	AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
	adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)	
	Length = 244	
Score = 458 (166.3 bits), Expect = 7.6e-44, P = 7.6e-44		
Identities = 102/204 (50%), Positives = 129/204 (63%)		
Query:	86	GIKGDQGSRGSPGKGPKGLAGPMGEKGLRGETGPQQGKGNKGDVGPTGPEGPRGNIGPL 145
	GI G G G+PG+ G G GEKG G GP KG+ G+ G EGPRG G	
Sbjct:	42	GIPGHPGHNGAPGRDGRDGTLIGP---KGDIGETGVPGAEGPRGFPGIQ 98
Query:	146	GPTGLPMPGPIGPKG-PKG-EAGPTGPQDMPIKFDKILYNBNHYDTAAGKFTCHIAGV 203
	G G PG + + G E T P +MP +F KI YN+ NHYD + GK F C+I G+	
Sbjct:	99	GRKGEPEGEGAYVYRSAFSVGLEYTYTIP-NMPPERFTKIFYNQNQHYDGSTGKFHNCNIPGL 157
Query:	204	YYFTYHITVFSRNVQVSLVKNGVKILHTKDAYSSE-DQASGGIVLQLKLGDEVWLQVTG 262
	YYF YHITV+ ++V+VSL K +L T D Y + DQASG + +L L+ +GD+VWLQV G	
Sbjct:	158	YYFAYHITVYVMKDVVKSLFKKDAMLFTYDQYQENNYYDQASGSVLLHLEVQDWLQVYVG 217
Query:	263	-GERFNGLFADEDDDTTFTGPLL 285
	GER NGL+AD D+D+TFTGFLL+	
Sbjct:	218	EEGER-NGLYADNDNDSTFTGFLLY 240

**FIG. 10**

## BLASTP ALIGNMENT OF SEQ ID NO: 215 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 215)  
 Subject: gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 208 (78.3 bits), Expect = 1.4e-16, P = 1.4e-16

Identities = 57/178 (32%), Positives = 86/178 (48%)

Query:	104 GLAGPMGEKGGLRGETGPQQKGKGNKGDVGPTGPEGPRGNIGPLGPTGLPGPMGPIGKPGPK 163
	G+ G G G+ G G G KG+ G G GP+G+ G G TG GP G G G K
Sbjct:	41 GIPGHPGHNGVPGRDGTPEKGEKGDPGLIGPKGDTGETGVGTGAEGPGRGFPGIQQRK 100

  

Query:	164 GEAGPTGQGEPGVR-GIRGWKGDRGEKGKIGETLVLPKSAFTYGLTVLSKFPSDDVPIK 222
	GE G G+ + + + ++ + G T KF + +
Sbjct:	101 GEPGEGAYVYRSAFVGLETTVPNMPIRFTKIFYNQQNHYD-GST--GKFHCNIPGLY 157

  

Query:	223 FDKIHITVFSRNVQVSLVKNGVKILHTRDAYVSSE-DQASGSIVLQLKLGDEMWCVIH 279
	+ HITV+ ++V+VSL K +L T D Y + DQASGS++L L+GD++W ++
Sbjct:	158 YFAYHITVYMKDVKKVSLFKKDAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVY 215

**FIG. 11**

**BLASTP ALIGNMENT OF SEQ ID NO: 215 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)**

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Query: Adiponectin-Like Polypeptide (SEQ ID NO: 215)
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
          adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 213 (80.0 bits), Expect = 7.0e-18, P = 7.0e-18

Identities = 60/182 (32%), Positives = 91/182 (50%)

Query: 104 GLAGPMGEKGGLRGETGPQGQKGNKGDVGGPTGPEGPRGNIGPLGPMPGPIGKPGPK 163
       G+ G   G   G   G   G   G   G   KG+ G   G   GP+G+IG   TG+PG   GP   G   PG   +
Sbjct:  42 GIPGHPGHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGE--TGVPGAEGPRGFPGIQ 98

Query: 164 GEAGPTGPQGEPGVRL--GIRGWKGDRGEKGKIGETLVLPKSAFTVGLTVLSKFPSSD 218
       G   G   G +G   R   G+   +   +   +   +   +   +   +   +
Sbjct:  99 GRKGEPE-EGAYVYRSAFSVGLEYTYTIPNMPPERFTKIFYNQONHYD-GST--GKFHCNI 154

Query: 219 VPIKFDKIHIITVFSRNVQVSLLVKNGVKILLHTRAYISSE-DQASGSIVLQLKLGDEMWCV 277
       +   +   HITV+ ++V+VSL K   +L T D Y   +   DQASGS++L L++GD++W
Sbjct: 155 PGLYYFAYHITVYMKDVKVSLLFKDKAMLFITYDQYQENNNYDQASGSVLLHLEVGDQVWLQ 214

Query: 278 IH 279
       ++
Sbjct: 215 VY 216

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F D E D 2 T m 6 F + 5 0 0 T

**BLASTP ALIGNMENT OF SEQ ID NO: 241 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)**

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 241)  
Subject: gi|5213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
Length = 243

Score = 476 (172.6 bits), Expect = 5.4e-45, P = 5.4e-45

Identities = 101/202 (50%), Positives = 129/202 (63%)

Query: 131 GPTGPEGPRGNIGPLGPTGLPGPMGPICKPKGEAGPTGPQGEVGIRGWKGDRGEK 190  
G G G G G PG G G PG G G PG G G TG G G +G RG+ G +G K  
Sbjct: 41 GIPGHPGHNGVPGRDGTPEKGEKGDPLIGPKDGTGETGVTGAEGPGRGFPGIQGRK 100

Query: 191 GKIGETLVLVLPKSAFTVGLTVLSKFSSDRPIKFDKILLYNEFNHYDTAAGKFTCHIAGYYY 250  
G+ GE + +SAF+VGL P+ PI+F KI YN+ NHYD + GKF C+I G+YY  
Sbjct: 101 GEPGEGAYVYRSAFSGLETTVVPNM - PIRFTKIFYNQQNHYDGSTGKFCNCNIPGLYY 158

Query: 251 FTYHITVFSRNVQVSIVKNGVKILHTKDAYMSSE-DOASGGIVLQLKLGDEVWLQVTG-G 308  
F YHITV+ ++V+VSL K +L T D Y + DQASG ++L L+GD+VWLQV G G  
Sbjct: 159 FAYHITVYMKDVVKVSLFKKDKAMLFTYDQYQENNNVDQASGSVLLHLEVGDQVWLQVYGEG 218

Query: 309 ERFNGLFADEDDDTTFTGFLLF 330  
ER NGL+AD D+D+TFTGFLL+  
Sbjct: 219 ER-NGLYADDNDNSTFTGFLLY 239

**FIG. 13**

**BLASTP ALIGNMENT OF SEQ ID NO: 241 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)**

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 241)  
 Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
 adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
 Length = 244

Score = 473 (171.6 bits), Expect = 2.0e-45, P = 2.0e-45

Identities = 100/202 (49%), Positives = 128/202 (63%)

Query:	131	GPTGPEGPRGNITGPLGPTGLPGPMGPIGKPGPKGEAGPTGPGQCEPGVQGIRGWKGDRGEK	190
	G G G G G PG G G PG G G PG G G PG +G RG+ G +G K		
Subject:	42	GIPGHPGHNGAPGRDDGRGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK	101

Query:	191	GKIGETLVLPKSAFTVGLTVLSKFSSDRPIKFDKILLYNEFNHYDTAAGKFTCHIAGVYY	250
	G+ GE + +SAP+VGL P+ P +F KI YN+ NHYD + GKPF C+I G+YY		
Subject:	102	GEPGEGAYVYRASFVGLEYTYTIPNM--PERFTKIFYNQQNHYDGSTGKPHCNIPGLYY	159

Query:	251	FTYHITVFSRNVQVSILVKNGVKILHTKDAYSSE-DQASGGIVLQLKLGDEVWLQVTG-G	308
	F YHITV+ ++V+VSL K +L T D Y + DQASG ++L L++GD+VWLQV G G		
Subject:	160	FAYHITVYMKDVVKVSLFKDKAMLFYDQYQENNYDQASGSVLLHLEVGDQWNLQVYGE	219

Query:	309	ERFNGLFADEDDDTTFTGFLFF	330
	ER NGL+AD D+D+TFTGFLL+		
Subject:	220	ER-NGLYADDNDNSTFTGFLLY	240

**FIG. 14**

THEORY & COMPUTATION

BLASTP ALIGNMENT OF SEQ ID NO: 272 WITH  
ADIPOSE TISSUE-SPECIFIC PROTEIN ADIPO Q (SEQ ID NO: 403)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 272)  
Subject: gi|4289336 AF269230\_1 (AF269230) adipose tissue-specific protein adipo Q  
[Bos taurus] (SEQ ID NO: 403) Length = 240

Score = 212 (79.7 bits), Expect = 1.0e-34, Sum P(2) = 1.0e-34

Identities = 41/78 (52%), Positives = 56/78 (71%)

Query: 227 HITVFSRNVQVSILVKNGVKILHTKDAYMSSE-DQASSGGIVLQLKLKGDEVWLQVTGGERFN 285  
HITV+ ++V+VSL K +L T D Y DQASG ++L L+GD+VWLQV GE N  
Sbjct: 158 HITVYMKDVKVSLFKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQWVLQVYEGENHN 217

Query: 286 GLFADEDDEDTTFTGFLLF 303  
G++AD +D+TFTGFLL+  
Sbjct: 218 GYYADNVNDSTFTGFLLY 235

FIG. 15a

FIGURE 15b

BLASTP ALIGNMENT OF SEQ ID NO: 272 WITH  
ADIPOSE TISSUE-SPECIFIC PROTEIN ADIPO Q (SEQ ID NO: 403)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 272)  
Subject: gi|4289336 AF269230\_1 (AF269230) adipose tissue-specific protein adipo Q  
[Bos taurus] (SEQ ID NO: 403) Length = 240

Score = 183 (69.5 bits), Expect = 1.0e-34, Sum P(2) = 1.0e-34

Identities = 43/100 (43%), Positives = 56/100 (56%)

Query: 6 LLLAIEIC TGNINSQD-----TCRQGHPGIPGIPGNPGHNGLPGRDGRDGAKGDKGDA GE PG 59  
LLL A+ G N +D C GIPG+PGHNG PGRDGRDG G+KG+ G+ G  
Sbjct: 9 LLLALP-SHGEDNMEDDPPLPKGACAGWMAGIPGHPGHNGTPGRDGRDGTPGEKGEKG DAG 67

Query: 60 RPGSPGKDGTSGEKGKGERGADGKVEAKGIKGQGSRGSPGK 99  
G G+ +G+ G GA+G +G G +G PG+  
Sbjct: 68 LLGPKGE--TGDVGMTGAEGP--RGFPGTPGRKGE PGE 101

FIG. 15b

**BLASTP ALIGNMENT OF SEQ ID NO: 272 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)**

Query:	Adiponectin-Like Polypeptide (SEQ ID NO: 272)	
Subject:	AY85144 AAY85144	13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
	adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)	
	Length = 244	
Score =	307 (113.1 bits), Expect = 7.6e-28, P = 7.6e-28	
Identities =	84/200 (42%), Positives = 109/200 (54%)	
Query:	131	GPTGPEGPRGNIGNPLGPTGLPGPMGPIGKPGPKGEAGPTEQGPGVQGIRGWKGDRGEK 190
	G G G G G G G PG G G PG G G PG G G PG +G RG+ G +G K	
Sbjct:	42	GIPGHGPNGAPGRDGRDGTPEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQGRK 101
Query:	191	GKIGETLVLPKSAFTVGLTVLSKFSS-DRPIK-----FD-----KIH----- 227
	G+ GE + SAF+VGL P+ +R K +D K H	
Sbjct:	102	GEPGEGAYVYRSAFSVGLEYTTIPNMPPERFTKIFYNQQNHYDGSTGKFCNCNIPGLYYFA 161
Query:	228	-ITVFSRNVQVSLVKNGVKILLHTKDAYMSE-DQASGGIVLQLKLGDEVNLQVTG-GER 283
	ITV+ ++V+VSL K +L T D Y + DQASG ++L L++GD+VWLQV G GER	
Sbjct:	162	YHITVYMKDVKVSLFKDKAMLLFTYDQYQENNYDQASGSVLLHLEVGDQWNLQVYGBGER 221
Query:	284	FNGLFADEDDDTTFTGFLLF 303
	NGL+AD D+D+TFTGFLL+	
Sbjct:	222	-NGLYADNDNDSTFTGFLLY 240

THEORY OF GENOTYPE

**BLASTP ALIGNMENT OF SEQ ID NO: 302 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)**

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 302)  
Subject: gi|5213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
Length = 243

Score = 330 (121.2 bits), Expect = 1.6e-29, P = 1.6e-29

Identities = 82/220 (37%), Positives = 116/220 (52%)

Query: 124 PSTAAATPDRGLMOSLPTFIQGPKEAGRPGKAGPRGPPGEPGPMPGMGPGEKGEPGRQG 183  
P A T G M +P G G GR G+ G GE G PG +GP G+ GE G G  
Sbjct: 31 PKGACT--GWMAGIPTH-PGHNNGVPGRDGRDGTGPGEKGKDPLIGPKGDTGETGYTG 86

Query: 184 LPGPPGAPGLNAA-GAISAATYSTGPKIAFYAGLKRQHEGYEV-LKFDDVVTNLGNHYDP 241  
GP G PG+ G Y + AF GL+ + ++F + N NHYD  
Sbjct: 87 AEGPRGFPGPQGRKRGKGEPEGAYVY-RSAFSVGLETYVTVPNMPIRFTKIFYQNQMHYDG 144

Query: 242 TTGKFTCSIPGIYFFTYHVLMRGGDTSWADLCKNNQVRASAIAQDADQNYDYASNSVV 301  
+TGKF C+IPG+Y+F YH+ + D + L K ++ Q + N D AS SV+  
Sbjct: 145 STGKFHCNIPGLYYFAHYITVYMKD---VKVSLFKDKAMLFYDQYQENNVDQASGSVL 201

Query: 302 LHLEPGDEVYIKLDG-GKAHG-GNNNKYSTFSGFIIYAD 338  
LHLE GD+V+++ G G+ +G +N+ STF+GF+Y D  
Sbjct: 202 LHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLJLYHD 241

**FIG. 17**

**BLASTP ALIGNMENT OF SEQ ID NO: 302 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)**

```

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 302)
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 336 (123.3 bits), Expect = 5.8e-31, P = 5.8e-31

Identities = 83/220 (37%), Positives = 117/220 (53%)

Query: 124 PSTAATPDRGLMOSLPTFIQGPCKGEAGRPGKAGPRGPPGEPGPPGMPPGEKGEPGRQG 183
P A T G M +P G G GR G+ G G GE G PG +GP G+ GE G G
Sbjct: 32 PKGACT--GWMAGIPGH-PGHNNGAPGRDGRDGTGPKGEKGDPGLIGPKGDIGETGVPG 87

Query: 184 LPGPPGAPGLNAA-GAISAATYSTSTGPKIAFYAGLKQHEGYEVIL-KFDDVVTVNLGNHYDP 241
GP G PG+ G Y + AF GL+ + + +F + N NHYD
Sbjct: 88 AEGPRGFPGPIQGRKKGEPGEAYVY--RSAFSVGLEYTYTIPNMPPERFTKIFYNQQNHYDG 145

Query: 242 TTGKFTCSIPGIYFFTYHVLMRGGDGTSMWADLCKNNQVRASAIAQDADQNYDYASNSVV 301
+TGKF C+IPG+Y+F YH+ + D + L K ++ Q + NYD AS SV+
Sbjct: 146 STGKFHCNIPGLYYFAHYITVYMKD---VIKVSLFKDKAMLFYTQYQENNYDQASGSVL 202

Query: 302 LHLEPGDEVYIKLDG-GKAHG--GNNNKYSTSGFIIYAD 338
LHLE GD+V+++ G G+ +G +N+ STF+GF++Y D
Sbjct: 203 LHLEVGDQVWLQVYGEGERGLYADNDNDSTFTGFLLYHD 242

```

**FIG. 18**

BLASTP ALIGNMENT OF SEQ ID NO: 323 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query:	Adiponectin-Like Polypeptide (SEQ ID NO: 323)	
Subject:	gi 15213856 AF404407_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)	
Length:	243	
Score:	330 (121.2 bits), Expect = 1.6e-29, P = 1.6e-29	
Identities:	82/220 (37%), Positives = 116/220 (52%)	
Query:	30	PSTAATPDRGLMQSLPTFIQGPKGEAGRPCKAGPRGGPPGEPGPPGPMGPGERGEPEGRQQ 89
P A T G M +P G G GR G+ G GE G PG +GP G+ GE G G		
Sbjct:	31	FKGACT--GWMAGIPGH-PGHNNGVPGRDGRDGTPGEKGEKGDPLIGPKGDTGETGVTG 86
Query:	90	LPGPPGAPGLNAA-GAISAATYSTGPKIAFYAGLKRQHEGYEV-LKFDDVVNLGNHYDP 147
GP G PG+ G Y + AF GL+ + +F + N NHYD		
Sbjct:	87	AEGPRGFPGIQRGRKGEPGEAYVY - RSAFSVGLETYYTVPNMPIRFTKIFYNQQNHYDG 144
Query:	148	TTGKFTCSIPGIYFFFTHVLMRGGDGTSMWADLCKNNQVRASAIQAQDADQNYDYASNSVV 207

Query:	208	LHLEPGDEVYIKLDG-GKAHG--GNNNKYSTFSGFIIYAD	244
		LHLE GD+V+++ G +G +N+ STF+GF++Y D	
Sbjct:	202	LHLEVGDQVNQLQVYGEGERNGLYADNDNDSTFTGFLLYHD	241

FIG. 19

BLASTP ALIGNMENT OF SEQ ID NO: 323 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 323)  
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 336 (123.3 bits), Expect = 5.8e-31, P = 5.8e-31

Identities = 83/220 (37%), Positives = 117/220 (53%)

Query: 30 PSTAAATPDRGLMQSLPTFIQGPGEAGRPGKAGPRGPPGEPGPPGPPGEKGEPEGRQG 89  
P A T G M +P G G GR G+ G G GE G PG +GP G+ GE G G  
Sbjct: 32 PKGACT--GWMAGIPIGH-PGHNNGAPGRDGRDGTGPKGEKGDPPGLIGPKGDIGETGVPG 87

Query: 90 LPGPPGAPGLNAA-GAISAATYSTGPKIAFYAGLKRQHEGYEVL-KFDDVVTVNLGNHYDP 147  
GP G PG+ G Y + AF GL+ + + +F + N NHYD  
Sbjct: 88 AEGPRGFPGPIQGRKKGEPGEAYVY-RSAFSVGLEYTYTIPNMMPERFTKIFYNQNQNYHDG 145

Query: 148 TTGKFTCSIPGIYFFTYHVLMRGDGTSMWADLCKNDNQVRASAIAQDADQNYDYASNSVV 207  
+TGKF C+IPG+Y+F YH+ + D + L K ++ Q + NYD AS SV+  
Sbjct: 146 STGKFPHCNIPGLYYFAFYHITVYMKD---VKVSLFKDKAMLFTYDQYQENNNYDQASGSVL 202

Query: 208 LHLEPGDEVYIKLDG-GKAHG--GNNNKYSTFSGFLIIYAD 244  
LHLE GD+V+++ G G+ +G +N+ STF+GF++Y D  
Sbjct: 203 LHLEVGDQWVLQVYGEGERNGLYADNDNDSTFTGFLLYHD 242

FIG. 20

**BLASTP ALIGNMENT OF SEQ ID NO: 348 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)**

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 348)  
Subject: gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
Length = 243

Score = 138 (53.6 bits), Expect = 1.9e-06, P = 1.9e-06

Identities = 69/220 (31%), Positives = 90/220 (40%)

Query: 296 PQQGSTGIVIAETGQAGPPAGAGVSGR -GLPRGVDFGGTGSCTVPPGAEGFAGAGPYPKSPP 354  
Sbjct: 43 PGHPGHNGVPGRDGRDGTPGEKGEKGDPGLI -GPKGDTGETGVTTGAEGPGRGFPGIQGRKG 101

Query: 355 VASPGAPVPSLVSFSAGL -TQKPFPSPDGGVVLFNKKVLVNDGDVYNPSTGVFTAPYDGRYL 413  
Sbjct: 102 EPGEGLAYVYRS -AFSVGLETYVTVPNMP - IRFTKIFFYNNQNHYDGSTGKFHCNIPGLYY 158

Query: 414 ITATLTPERDAYVEAV -LSVSNASAQLHTAGYRREFLEYHRPTGALHTCCGGPAFHLLIV 472  
Sbjct: 159 FAYHIT ---VYMKDVKVSLFKDKAMLF T--Y----DQYQENNVDQASGS-----VLL 202

Query: 473 HIKAGDAVNVVVTG -----GKLAHTDFDEMYSFGVFLY 507  
Sbjct: 203 HLEVGDQWVLQVYGEGERNGLYADNDND ---STFTGFELLY 239

**FIG. 21**

**BLASTP ALIGNMENT OF SEQ ID NO: 348 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)**

```

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 348)
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 132 (51.5 bits), Expect = 1.7e-06, P = 1.7e-06

Identities = 75/243 (30%), Positives = 98/243 (40%)

Query: 269 PRPSGPATAEDPGRRPVLPQRPPEERPPQPPGSTGVIAETGQAGPPAGAGVSGRGLPRGV 328
P P G T G +P P G G E G+ G P G+ G P+G
Sbjct: 30 PLPKGACTGWMAG---LPGHPGHNGAPGRDGRDGTPGEKGEKGDP---GLIG---PKG D 79

Query: 329 DGQTGSCTVPGAAEGFAGAPGYPKSPPVAVSPGAPVPSLVSFSAGL-TQKPPPSDGGVVLFN 387
G+TG VPGAEQ G PG GA V +FS GL T P+
Sbjct: 80 IGETG---VPGAEQPRGFPGFQGRKGEPEGAYVYRS-AFSVGLETYYTIPNMPE-RFT 133

Query: 388 KVLVNDGDVYNPSTGVFTAPYDGRYLITATLPERDAYVEAV-LSVSNASVAAQLHTAGYR 446
K+ N + Y+ STG F G Y +T Y++ V +S+ A L T
Sbjct: 134 KIFYNQQNHYDGSTGKFHCNIPGLYYFAYHIT----VYMKDVKVSLFKKDKAMLFTYDQY 189

Query: 447 REFLEYHRPTGA--LHTCGGPGAFHLIVHLKAGDAVNVVVTGGKLAHTDFDEMYSFGV 504
+E Y + +G+ LH G + L V+ G+ G A D D STE+G
Sbjct: 190 QEN-NYDQASGSVLLHLEVGDQVW-LQVY--GEGER----NGLYADNDND---STFTGF 237

Query: 505 FLY 507
Sbjct: 238 LLY 240

```

BLASTP ALIGNMENT OF SEQ ID NO: 355 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 355)  
Subject: gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
Length = 243

Score = 199 (75.1 bits), Expect = 1.2e-15, P = 1.2e-15

Identities = 53/134 (39%), Positives = 68/134 (50%)

Query: 37 PRGPGPDGAPASVPPFP-----PGAKGEVRRGKAGLRGPPGPPGPRGPGRPGPPG 91  
Sbjct: P+G G A +P P PG G G+ G +G PG GP+G GE G G G  
31 PKG-ACTGWMAGIPGHPGHNGVPGRDGRDGTGPKGDTGETGVTGAEG 89

Query: 92 PPG-PGPGGVA- -PAAG-YVPRIAFYAGLRRPHEGYEV-LRFDDVVTVGNAYEAASGKF 146  
Sbjct: P G PG G P G YV R AF GL + +RF + N N Y+ ++GKF  
90 PRGFPGIQGRKGEPEGEGAYVYRSAFSVGLETYVTPNMPIRFTKIFYNQONHYDGSTGKF 149

Query: 147 TCPMPGVYFFAYHV 160  
Sbjct: C +PG+Y+FAZH+  
150 HCNIPGLYYFAYHI 163

FIG. 23

**BLASTP ALIGNMENT OF SEQ ID NO: 355 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)**

```

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 355)
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length = 244

Score = 204 (76.9 bits), Expect = 6.3e-17, P = 6.3e-17

Identities = 54/134 (40%), Positives = 69/134 (51%)

Query: 37 PRGPGPDGAPASVPPPFP-----PGAKGEYGRRKGAGLRLRGGPPGPRGPGEPRGPPG 91
P+G G A +P P PG G G G+ G +G PG GP+G GE G PG G
Sbjct: 32 PKG-ACTGWMAGIPGHNGAPGRDGRDGTPEKGEKGDPGGLIGPKGDIGETGVPGAEQ 90

Query: 92 PPG-PPGGVA - PAAG-YVPRIAFYAGLRRPHEGYEVL-RFDDVVTVGNAYEAASGKF 146
P G PG G P G IV R AF GL + + RF + N N Y+ ++GKF
Sbjct: 91 PRGFPGIQQGRKGEPGEGAYVYRSSAFSVGLETYYTIPNMPERFTKIFYNQQNHYDGSTGKF 150

Query: 147 TCPMPGVYFFAYHV 160
Sbjct: 151 HCNIPGLYYFAYHI 164

```

## BLASTP ALIGNMENT OF SEQ ID NO: 378 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 378)  
 Subject: gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 297 (109.6 bits), Expect = 5.0e-26, P = 5.0e-26

Identities = 80/215 (37%), Positives = 113/215 (52%)

Query: 37 PRGPGPDGAPASVPPFP-----PGAKGEVRRGKAGLRLRGGPPGPPGPRGPGEPRGPGPPG 91  
 Sbjct: P+G G A +P P PG G G+ G +G PG GP+G GE G G G

Query: 31 PKG-ACTGWMAGIPGHPGHNGVPGRDGRDGTGPKGDTGETGVTGAEG 89

Query: 92 PPG-PGPGVVA- -PAAG-YVPRIAFYAGLRRPHEGYEV-LRFDDVVTVGNAYEAASGKF 146  
 Sbjct: P G PG G P G YV R AF GL + +RF + N N Y+ ++GKF

Query: 90 PRGFPGIQQGRKGEPGEGAYVRSAFSVGLLETYVTPNMPIRFTKIFYNQONHYDGSTGKF 149

Query: 147 TCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIQDADQNYDYASNSVILHLDV 206  
 Sbjct: C +PG+Y+FAYH+ + D + L K + Q + N D AS SV+LHL+V

Query: 150 HCNIPGLYYFAYHITVYMKD ---VKVSLFKKDAMLFTYDQYQENNNVDQASGSVLLHIEV 206

Query: 207 GDEVFIKLDG-GKVHG--GNTNKYSTFSGFIYPD 238  
 Sbjct: GD+V+++ G G+ +G + STF+GF+Y D

Query: 207 GDQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 241

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BLASTP ALIGNMENT OF SEQ ID NO: 378 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 378)  
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 310 (114.2 bits), Expect = 3.7e-28, P = 3.7e-28

Identities = 82/215 (38%) , Positives = 115/215 (53%)

Query :	92	PPG-PGGGVAA--PAAG-YVPIRAFYAGLRRPHEGYEVL-RFDVVTVNGNAYEAASGKF	146
	P G PG G P G YV R AF GL + + RF + N N.Y+ ++GKF		
subjct :	91	PRGFPGIQQRKGEPEGAYVYRASFVGLEYTYTIPNMPERFTKIFYNOONHYDGSTGKF	150

Query:	147	TCPMPGVYFFAYHVLMRGDDGTSMWADLMKNGQVRASAIQDADQNYDYASNSVILHLDV	206
	C +PG+Y +FA YH+ +	D + L K + Q + NYD AS SV+LHL+V	
Sbjct:	151	HCNTPGIYLYFAHTTIVYMKD-- -VKVYSTLEKKDKAMIEFVYDOYOENNMDOMSCSVLUVEN	207

Query : 207 GDEVFIKLDG-GKVHG--GNTNKGYSTFSGFIIYYPD 238  
GD+V+++ G + + + STF+GF+Y D